Phyre2

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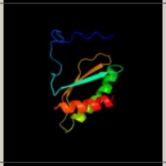
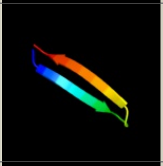
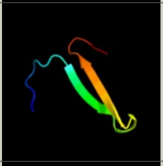
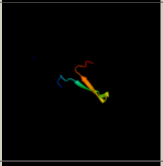
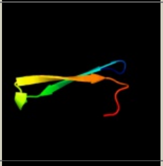
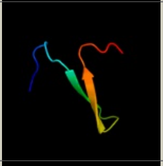
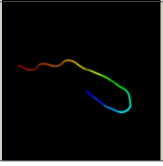
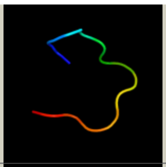
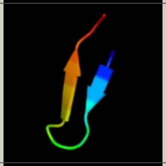
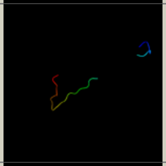
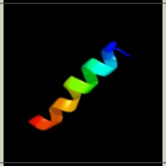
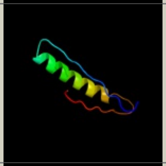
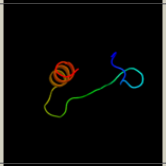
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2k3iA_	Alignment		100.0	99	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein yiis; **PDBTitle:** solution nmr structure of protein yiis from shigella2 flexneri. northeast structural genomics consortium target3 sfr90
2	c2khdA_	Alignment		100.0	32	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein vc_a0919; **PDBTitle:** solution nmr structure of vc_a0919 from vibrio cholerae.2 northeast structural genomics consortium target vcr52
3	c2jz5A_	Alignment		100.0	35	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein vpa0419; **PDBTitle:** nmr solution structure of protein vpa0419 from vibrio2 parahaemolyticus. northeast structural genomics target3 vpr68
4	c2c60A_	Alignment		22.8	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**human mitogen-activated protein kinase kinase **PDBTitle:** crystal structure of human mitogen-activated protein kinase2 kinase kinase 3 isoform 2 phox domain at 1.25 a resolution
5	d2czra1	Alignment		20.8	36	**Fold:**Restriction endonuclease-like **Superfamily:**TBP-interacting protein-like **Family:**TBP-interacting protein-like
6	c3gitA_	Alignment		14.6	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**carbon monoxide dehydrogenase/acetyl-coa synthase subunit **PDBTitle:** crystal structure of a truncated acetyl-coa synthase
7	d1oaoc_	Alignment		13.3	21	**Fold:**Prismane protein-like **Superfamily:**Prismane protein-like **Family:**Acetyl-CoA synthase
8	c3s2xB_	Alignment		12.6	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**acetyl-coa synthase subunit alpha; **PDBTitle:** structure of acetyl-coenzyme a synthase alpha subunit c-terminal2 domain
9	d2v4ja1	Alignment		12.2	35	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
10	d1ru3a_	Alignment		11.5	17	**Fold:**Prismane protein-like **Superfamily:**Prismane protein-like **Family:**Acetyl-CoA synthase
11	d1k81a_	Alignment		9.9	29	**Fold:**Zinc-binding domain of translation initiation factor 2 beta **Superfamily:**Zinc-binding domain of translation initiation factor 2 beta **Family:**Zinc-binding domain of translation initiation factor 2 beta

12	d2d8xa2	Alignment		9.6	50	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
13	d2fiya1	Alignment		9.2	8	**Fold:**FdhE-like **Superfamily:**FdhE-like **Family:**FdhE-like
14	c2k8eA_	Alignment		9.0	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0339 protein yegp; **PDBTitle:** solution nmr structure of protein of unknown function yegp from e.2 coli. ontario center for structural proteomics target ec0640_1_1233 northeast structural genomics consortium target et102.
15	c3cngC_	Alignment		8.8	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nudix hydrolase; **PDBTitle:** crystal structure of nudix hydrolase from nitrosomonas europaea
16	c2o6nA_	Alignment		7.8	24	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**rh4b designed peptide; **PDBTitle:** rh4b: designed right-handed coiled coil tetramer with all biological2 amino acids
17	d1r3na2	Alignment		7.8	6	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
18	d2ctka1	Alignment		7.6	11	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
19	d1xxaa_	Alignment		7.0	15	**Fold:**DCoH-like **Superfamily:**C-terminal domain of arginine repressor **Family:**C-terminal domain of arginine repressor
20	d1dl6a_	Alignment		6.9	22	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
21	c3cagF_	Alignment	not modelled	6.6	16	**PDB header:**dna binding protein **Chain:** F: **PDB Molecule:**arginine repressor; **PDBTitle:** crystal structure of the oligomerization domain hexamer of the2 arginine repressor protein from mycobacterium tuberculosis in complex3 with 9 arginines.
22	c3uajA_	Alignment	not modelled	6.4	8	**PDB header:**viral protein/immune system **Chain:** A: **PDB Molecule:**envelope protein; **PDBTitle:** crystal structure of the envelope glycoprotein ectodomain from dengue2 virus serotype 4 in complex with the fab fragment of the chimpanzee3 monoclonal antibody 5h2
23	c3i08D_	Alignment	not modelled	6.2	30	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**neurogenic locus notch homolog protein 1; **PDBTitle:** crystal structure of the s1-cleaved notch1 negative2 regulatory region (nrr)
24	c2jyaA_	Alignment	not modelled	6.2	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu1810; **PDBTitle:** nmr solution structure of protein atu1810 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr23,3 ontario centre for structural proteomics target atc1776
25	d3c7ba1	Alignment	not modelled	6.2	35	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
26	c2k2dA_	Alignment	not modelled	6.1	25	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**ring finger and chy zinc finger domain- **PDBTitle:** solution nmr structure of c-terminal domain of human pirh2.2 northeast structural genomics consortium (nesg) target ht2c
27	d1rutx2	Alignment	not modelled	5.9	54	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain

28	d3d3ra1	Alignment	not modelled	5.8	15	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
29	c3h0gL_	Alignment	not modelled	5.5	25	**PDB header:**transcription **Chain:** L: **PDB Molecule:**dna-directed rna polymerases i, ii, and iii **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe